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RAW SEQUENCE LISTING DATE: 01/28/2004
PATENT APPLICATION: **US/09/856,339B** TIME: 10:42:28

Input Set : **A:\P02196US0.txt**
Output Set: **N:\CRF4\01282004\I856339B.raw**


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  3 <110> APPLICANT: Wong, Luet
  5 <120> TITLE OF INVENTION: Process for oxidising terpenes
  7 <130> FILE REFERENCE: P02196US0
  9 <140> CURRENT APPLICATION NUMBER: US 09/856,339B
C--> 10 <141> CURRENT FILING DATE: 2001-08-15
 12 <150> PRIOR APPLICATION NUMBER: PCT/GB99/03873
 13 <151> PRIOR FILING DATE: 1998-11-19
 15 <160> NUMBER OF SEQ ID NOS: 24
 17 <170> SOFTWARE: PatentIn version 3.1
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 1242
 21 <212> TYPE: DNA
 22 <213> ORGANISM: Pseudomonas putida
 24 <220> FEATURE:
 25 <221> NAME/KEY: misc_feature
 26 <222> LOCATION: (1)..(1242)
 27 <223> OTHER INFORMATION: Coding Sequence
 30 <400> SEQUENCE: 1
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 33 cacctggtat tcgacttcga catgtacaat ccgtcgaatc tgtctgccgg cgtgcaggag    120
 35 gcctgggcag ttctgcaaga atcaaacgta ccggatctgg tgtggactcg ctgcaacggc    180
 37 ggacactgga tcgccactcg cggccaactg atccgtgagg cctatgaaga ttaccgccac    240
 39 ttttccagcg agtgcccgtt catccctcgt gaagccggcg aagcctacga cttcattccc    300
 41 acctcgatgg atccgcccga gcagcgccag tttcgtgcgc tggccaacca agtggttggc    360
 43 atgccggtgg tggataagct ggagaaccgg atccaggagc tggcctgctc gctgatcgag    420
 45 agcctgcgcc cgcaaggaca gtgcaacttc accgaggact acgccgaacc cttcccgata    480
 47 cgcatcttca tgctgctcgc aggtctaccg gaagaagata tcccgcactt gaaataccta    540
 49 acggatcaga tgacccgtcc ggatggcagc atgaccttcg cagaggccaa ggaggcgctc    600
 51 tacgactatc tgataccgat catcgagcaa cgcaggcaga agccgggaac cgacgctatc    660
 53 agcatcgttg ccaacggcca ggtcaatggg cgaccgatca ccagtgacga agccaagagg    720
 55 atgtgtggcc tgttactggt cggcggcctg gatacggtgg tcaatttcct cagcttcagc    780
 57 atggagttcc tggccaaaag cccggagcat cgccaggagc tgatcgagcg tcccgagcgt    840
 59 attccagccg cttgcgagga actactccgg cgcttctcgc tggttgccga tggccgcatc    900
 61 ctcacctccg attacgagtt tcatggcgtg caactgaaga aaggtgacca gatcctgcta    960
 63 ccgcagatgc tgtctggcct ggatgagcgc gaaaacgcct gcccgatgca cgtcgacttc   1020
 65 agtcgccaaa aggtttcaca caccaccttt ggccacggca gccatctgtg ccttggccag   1080
 67 cacctggccc gccgggaaat catcgtcacc ctcaaggaat ggctgaccag gattcctgac   1140
 69 ttctccattg ccccgggtgc ccagattcag cacaagagcg gcatcgtcag cggcgtgcag   1200
 71 gcactccctc tggtctggga tccggcgact accaaagcgg ta                      1242
 74 <210> SEQ ID NO: 2
 75 <211> LENGTH: 3150
 76 <212> TYPE: DNA
 77 <213> ORGANISM: Bacillus megaterium
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79 <220> FEATURE:
80 <221> NAME/KEY: misc_feature
81 <222> LOCATION: (1)..(3150)
82 <223> OTHER INFORMATION: Coding Sequence
85 <400> SEQUENCE: 2
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88 ttaaacacag ataaaccggt tcaagctttg atgaaaattg cggatgaatt aggagaaatc 120
90 tttaaattcg aggcgcctgg tcgtgtaacg cgctacttat caagtcagcg tctaattaaa 180
92 gaagcatgcg atgaatcacg ctttgataaa aacttaagtc aagcgcttaa atttgtacgt 240
94 gattttgcag gagacgggtt atttacaagc tggacgcatg aaaaaaattg gaaaaaagcg 300
96 cataatatct tacttccaag cttcagtcag caggcaatga aaggctatca tgcgatgatg 360
98 gtcgatatcg ccgtgcagct tgttcaaaag tgggagcgtc taaatgcaga tgagcatatt 420
100 gaagtaccgg aagacatgac acgtttaacg cttgatacaa ttggtctttg cggctttaac 480
102 tatcgcttta acagctttta ccgagatcag cctcatccat ttattacaag tatggtccgt 540
104 gcactggatg aagcaatgaa caagctgcag cgagcaaatc cagacgaccc agcttatgat 600
106 gaaaacaagc gccagtttca agaagatatc aaggtgatga acgacctagt agataaaatt 660
108 attgcagatc gcaaagcaag cggtgaacaa agcgatgatt tattaacgca tatgctaaac 720
110 ggaaaagatc cagaaacggg tgagccgctt gatgacgaga acattcgcta tcaaattatt 780
112 acattcttaa ttgcgggaca cgaaacaaca agtggtcttt tatcatttgc gctgtatttc 840
114 ttagtgaaaa atccacatgt attacaaaaa gcagcagaag aagcagcacg agttctagta 900
116 gatcctgctc caagctacaa acaagtcaaa cagcttaaat atgtcggcat ggtcttaaac 960
118 gaagcgctgc gcttatggcc aactgctcct gcgttttccc tatatgcaaa agaagatacg 1020
120 gtgcttggag gagaatatcc tttagaaaaa ggcgacgaac taatggttct gattcctcag 1080
122 cttcaccgtg ataaaacaat ttggggagac gatgtggaag agttccgtcc agagcgtttt 1140
124 gaaaatccaa gtgcgattcc gcagcatgcg tttaaaccgt ttggaaacgg tcagcgtgcg 1200
126 tgtatcggtc agcagttcgc tcttcatgaa gcaacgctgg tacttggtat gatgctaaaa 1260
128 cactttgact ttgaagatca tacaaactac gagctggata ttaaagaaac tttaacgtta 1320
130 aaacctgaag gctttgtggt aaaagcaaaa tcgaaaaaaa ttccgcttgg cggtattcct 1380
132 tcacctagca ctgaacagtc tgccaaaaaa gcacgcaaaa aggcagaaaa cgctcataat 1440
134 acgccgctgc ttgtgctata cggttcaaat atgggaacag ctgaaggaac ggcgcgtgat 1500
136 ttagcagata ttgcaatgag caaaggattt gcaccgcagg tcgcaacgct tgattcacac 1560
138 gccggaaatc ttccgcgcga aggagctgta ttaattgtaa cggcgtctta taacggtcat 1620
140 ccgcctgata acgcaaagca atttgtcgac tggttagacc aagcgtctgc tgatgaagta 1680
142 aaaggcgttc gctactccgt atttggatgc ggcgataaaa actgggctac tacgtatcaa 1740
144 aaagtgcctg cttttatcga tgaaacgctt gccgctaaag gggcagaaaa catcgctgac 1800
146 cgcggtgaag cagatgcaag cgacgacttt gaaggcacat atgaagaatg gcgtgaacat 1860
148 atgtggagtg acgtagcagc ctactttaac ctcgacattg aaaacagtga agataataaa 1920
150 tctactcttt cacttcaatt tgtcgacagc gccgcggata tgccgcttgc gaaaatgcac 1980
152 ggtgcgtttt caacgaacgt cgtagcaagc aaagaacttc aacagccagg cagtgcacga 2040
154 agcacgcgac atcttgaaat tgaacttcca aaagaagctt cttatcaaga aggagatcat 2100
156 ttaggtgtta ttcctcgcaa ctatgaagga atagtaaacc gtgtaacagc aaggttcggc 2160
158 ctagatgcat cacagcaaat ccgtctggaa gcagaagaag aaaaattagc tcatttgcca 2220
160 ctcgctaaaa cagtatccgt agaagagctt ctgcaatacg tggagcttca agatcctgtt 2280
162 acgcgcacgc agcttcgcgc aatggctgct aaaacggtct gcccgccgca taaagtagag 2340
164 cttgaagcct tgcttgaaaa gcaagcctac aaagaacaag tgctggcaaa acgtttaaca 2400
166 atgcttgaac tgcttgaaaa atacccggcg tgtgaaatga aattcagcga atttatcgcc 2460
168 cttctgccaa gcatacgccc gcgctattac tcgatttctt catcacctcg tgtcgatgaa 2520
170 aaacaagcaa gcatcacggt cagcgttgtc tcaggagaag cgtggagcgg atatggagaa 2580
172 tataaaggaa ttgcgtcgaa ctatcttgcc gagctgcaag aaggagatac gattacgtgc 2640

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174 tttatttcca caccgcagtc agaatttacg ctgccaaaag accctgaaac gccgcttatc   2700
176 atggtcggac cgggaacagg cgtcgcgccg tttagaggct ttgtgcaggc gcgcaaacag   2760
178 ctaaaagaac aaggacagtc acttggagaa gcacatttat acttcggctg ccgttcacct   2820
180 catgaagact atctgtatca agaagagctt gaaaacgccc aaagcgaagg catcattacg   2880
182 cttcataccg ctttttctcg catgccaaat cagccgaaaa catacgttca gcacgtaatg   2940
184 gaacaagacg gcaagaaatt gattgaactt cttgatcaag gagcgcactt ctatatttgc   3000
186 ggagacggaa gccaaatggc acctgccgtt gaagcaacgc ttatgaaaag ctatgctgac   3060
188 gttcaccaag tgagtgaagc agacgctcgc ttatggctgc agcagctaga agaaaaaggc   3120
190 cgatacgcaa aagacgtgtg ggctgggtaa                                   3150
193 <210> SEQ ID NO: 3
194 <211> LENGTH: 7
195 <212> TYPE: PRT
196 <213> ORGANISM: Artificial Sequence
198 <220> FEATURE:
199 <223> OTHER INFORMATION: Linker
201 <220> FEATURE:
202 <221> NAME/KEY: DOMAIN
203 <222> LOCATION: (1)..(7)
204 <223> OTHER INFORMATION: Linker
207 <400> SEQUENCE: 3
209 Thr Asp Gly Thr Ser Ser Thr
210 1               5
213 <210> SEQ ID NO: 4
214 <211> LENGTH: 7
215 <212> TYPE: PRT
216 <213> ORGANISM: Artificial Sequence
218 <220> FEATURE:
219 <223> OTHER INFORMATION: Linker
221 <220> FEATURE:
222 <221> NAME/KEY: DOMAIN
223 <222> LOCATION: (1)..(7)
224 <223> OTHER INFORMATION: Linker
227 <400> SEQUENCE: 4
229 Thr Asp Gly Ala Ser Ser Ser
230 1               5
233 <210> SEQ ID NO: 5
234 <211> LENGTH: 17
235 <212> TYPE: PRT
236 <213> ORGANISM: Artificial Sequence
238 <220> FEATURE:
239 <223> OTHER INFORMATION: Linker
241 <220> FEATURE:
242 <221> NAME/KEY: DOMAIN
243 <222> LOCATION: (1)..(17)
244 <223> OTHER INFORMATION: Linker
247 <400> SEQUENCE: 5
249 Thr Asp Gly Thr Arg Pro Gly Pro Gly Pro Gly Pro Gly Pro Ser Ser
250 1               5                  10                  15
253 Thr
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Input Set : **A:\P02196US0.txt**
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257 <210> SEQ ID NO: 6
258 <211> LENGTH: 21
259 <212> TYPE: PRT
260 <213> ORGANISM: Artificial Sequence
262 <220> FEATURE:
263 <223> OTHER INFORMATION: Linker
265 <220> FEATURE:
266 <221> NAME/KEY: DOMAIN
267 <222> LOCATION: (1)..(21)
268 <223> OTHER INFORMATION: Linker
271 <400> SEQUENCE: 6
273 Thr Asp Gly Thr Arg Pro Gly Pro Gly Pro Gly Pro Gly Pro Gly Pro
274 1 5 10 15
277 Gly Pro Ser Ser Thr
278 20
281 <210> SEQ ID NO: 7
282 <211> LENGTH: 4
283 <212> TYPE: PRT
284 <213> ORGANISM: Artificial Sequence
286 <220> FEATURE:
287 <223> OTHER INFORMATION: Linker
289 <220> FEATURE:
290 <221> NAME/KEY: DOMAIN
291 <222> LOCATION: (1)..(4)
292 <223> OTHER INFORMATION: Linker
295 <400> SEQUENCE: 7
297 Pro Leu Glu Leu
298 1
301 <210> SEQ ID NO: 8
302 <211> LENGTH: 7
303 <212> TYPE: PRT
304 <213> ORGANISM: Artificial Sequence
306 <220> FEATURE:
307 <223> OTHER INFORMATION: Linker
309 <220> FEATURE:
310 <221> NAME/KEY: DOMAIN
311 <222> LOCATION: (1)..(7)
312 <223> OTHER INFORMATION: Linker
315 <400> SEQUENCE: 8
317 Thr Asp Gly Gly Ser Ser Ser
318 1 5
321 <210> SEQ ID NO: 9
322 <211> LENGTH: 51
323 <212> TYPE: DNA
324 <213> ORGANISM: Artificial Sequence
326 <220> FEATURE:
327 <223> OTHER INFORMATION: Primer
329 <220> FEATURE:
330 <221> NAME/KEY: misc_feature

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Input Set : **A:\P02196US0.txt**
Output Set: **N:\CRF4\01282004\I856339B.raw**

331 <222> LOCATION: (1)..(51)
332 <223> OTHER INFORMATION: Primer
335 <400> SEQUENCE: 9
336 gagattaaga attcataaac acatgggagt gcgtgccata tgaacgcaaa c 51
339 <210> SEQ ID NO: 10
340 <211> LENGTH: 36
341 <212> TYPE: DNA
342 <213> ORGANISM: Artificial Sequence
344 <220> FEATURE:
345 <223> OTHER INFORMATION: Coding Sequence
347 <220> FEATURE:
348 <221> NAME/KEY: variation
349 <222> LOCATION: (1)..(36)
350 <223> OTHER INFORMATION: Desired coding sequence
353 <400> SEQUENCE: 10
354 gaactgagta gtgccactga cggaggatcc tcatcg 36
357 <210> SEQ ID NO: 11
358 <211> LENGTH: 36
359 <212> TYPE: DNA
360 <213> ORGANISM: Artificial Sequence
362 <220> FEATURE:
363 <223> OTHER INFORMATION: Primer
365 <220> FEATURE:
366 <221> NAME/KEY: misc_feature
367 <222> LOCATION: (1)..(36)
368 <223> OTHER INFORMATION: Primer
371 <400> SEQUENCE: 11
372 cgatgaggat cctccgtcag tggcactact cagttc 36
375 <210> SEQ ID NO: 12
376 <211> LENGTH: 36
377 <212> TYPE: DNA
378 <213> ORGANISM: ARTIFICIAL SEQUENCE
380 <220> FEATURE:
381 <223> OTHER INFORMATION: Primer
383 <220> FEATURE:
384 <221> NAME/KEY: misc_feature
385 <222> LOCATION: (1)..(36)
386 <223> OTHER INFORMATION: Primer
389 <400> SEQUENCE: 12
390 tcatcgggat cctcatcgat gtctaaagta gtgtat 36
393 <210> SEQ ID NO: 13
394 <211> LENGTH: 52
395 <212> TYPE: DNA
396 <213> ORGANISM: Artificial Sequence
398 <220> FEATURE:
399 <223> OTHER INFORMATION: Desired Coding Sequence
401 <220> FEATURE:
402 <221> NAME/KEY: misc_feature
403 <222> LOCATION: (1)..(52)

VERIFICATION SUMMARY DATE: 01/28/2004
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L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date